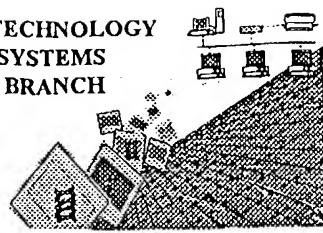# RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _10/089,211A_

Source: _1FWl6_

Date Processed by STIC: _9/17/04_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT
MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 4.2 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 06/05/04): U.S. Patent and Trademark Office, 220 20th Street S., Customer Window, Mail Stop Sequence, Crystal Plaza Two, Lobby, Room 1B03, Arlington, VA 22202

Revised 05/17/04

Raw Sequence Listing Error Summary

ERROR DETECTED   **SUGGESTED CORRECTION**   SERIAL NUMBER: _10/089, 211A_

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1_____Wrapped Nucleics   The number/text at the end of each line "wrapped" down to the next line. This may occur if your file
    Wrapped Aminos   was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will
     prevent "wrapping."

2_____Invalid Line Length   The rules require that a line **not exceed** 72 characters in length. This includes white spaces.

3_____Misaligned Amino   The numbering under each 5th amino acid is misaligned. Do **not** use tab codes between numbers;
    Numbering   use **space characters**, instead.

4_____Non-ASCII   The submitted file was **not** saved in ASCII(DOS) text, as **required** by the Sequence Rules. **Please
ensure your subsequent submission is saved in ASCII text.**

5_____Variable Length   Sequence(s)____contain n's or Xaa's representing more than one residue. **Per Sequence Rules,
each n or Xaa can only represent a single residue.** Please present the **maximum** number of each
residue having variable length and indicate in the <220>-<223> section that some may be missing.

6_____PatentIn 2.0   A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
    "bug"   sequences(s) _____. Normally, PatentIn would automatically generate this section from the
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to
the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for
Artificial or Unknown sequences.**

7_____Skipped Sequences   Sequence(s) _____ missing. If intentional, please insert the following lines for **each** skipped sequence:
    (OLD RULES)   (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
    (i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
    (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
    This sequence is intentionally skipped

    Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to **include** the skipped sequences.

8_____Skipped Sequences   Sequence(s) _____ missing. If **intentional**, please insert the following lines for **each** skipped sequence.
    (NEW RULES)   <210> sequence id number
    <400> sequence id number
    000

9_____Use of n's or Xaa's   Use of n's and/or Xaa's have been detected in the Sequence Listing.
    (NEW RULES)   Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
    In <220> to <223> section, please explain location of **n** or **Xaa**, and which residue n or Xaa represents.

10_____Invalid <213>   Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or
    Response   scientific name (Genus/species). <220>-<223> section is **required** when <213> response is Unknown or
is Artificial Sequence

11_____Use of <220>   Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses.
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or
"Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

12_____PatentIn 2.0   Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file,
    "bug"   resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence
listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13_____Misuse of n/Xaa   "n" can **only** represent a single <u>nucleotide</u>; "Xaa" can **only** represent a single <u>amino acid</u>

RAW SEQUENCE LISTING   DATE: 09/17/2004
PATENT APPLICATION: US/10/089,211A   TIME: 10:04:37

Input Set : A:\62447.txt
Output Set: N:\CRF4\09172004\J089211A.raw

```
 3 <110> APPLICANT: University of Victoria Innovation and Developement Corporation
 4        Hintz, William E.
 5        Eades, Caleb Joshua
 7 <120> TITLE OF INVENTION: Mannosidases and Methods for using the Same
 9 <130> FILE REFERENCE: 2847-62447-01
11 <140> CURRENT APPLICATION NUMBER: 10/089,211A
12 <141> CURRENT FILING DATE: 2002-03-25
14 <150> PRIOR APPLICATION NUMBER: PCT/US00/27210
15 <151> PRIOR FILING DATE: 2000-10-02
17 <150> PRIOR APPLICATION NUMBER: 60/157,341
18 <151> PRIOR FILING DATE: 1999-10-01
20 <160> NUMBER OF SEQ ID NOS: 19
22 <170> SOFTWARE: PatentIn version 3.1
24 <210> SEQ ID NO: 1
25 <211> LENGTH: 3328
26 <212> TYPE: DNA
27 <213> ORGANISM: Aspergillus nidulans
29 <400> SEQUENCE: 1
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32 taattctggg gaccgatatc ccttgaacgc gggggcaatc agttcaacca acccagaccg  120
34 ctgggcttgg tatgagattg cgagcatcta tgtcggtgta ccttctgaat gacaatgaat  180
36 gtattttact tctcgaaaag aacccttggg cactgaattg tgcggagaat gatgccctga  240
38 ttatgataca actagtccgc tccgtcaagc cacaagggtc tgggcagtcc gctataaatc  300
40 aaaatcgcct gcacgaacag acgaataacc aagaaaacgc ccgagcgcga gcgtttcttc  360
42 ttcctctaag ccttgcagct ggctctgcgt ctttgatcaa ccctttagct gaatttcccc  420
44 agaacttcag ccctctgcat cctgtcctta ccgcaactcg ttaacctgcg cgacctcgcg  480
46 cgaccacagc cttaggtttc gagatgccat gaaaatcaga aattgaaccc cctttccatt  540
48 actatcattc tctgcattct gcgagtgatc tgtccttcga cgttccttct ttccagcgct  600
50 gcggcgcctt cactctcgtt gcctacgttt gaccacggtc ctacctctcc tactgctgat  660
52 tattaggctc ctccctacgc ctccaataca gggaagtcgc cggccatgtt tcgtgcacga  720
54 cgatctcgca tctcgctggt gtttgccgtt atatttgtcc tcctcatatt ccactttagc  780
56 cgtctcgcag ttacgatcag cctgcaatct tgggtacctc cgccgcccgt cgatcaccat  840
58 aatccccctt tccccgacca gaacctcaaa gatccatacg aaaacgacaa tagtgcgacc  900
60 ggcagtgggg ctcctccgcc tgcgttggta gagccagaag aataccaacg accaccactt  960
62 tacacagatt cagatgacag cccaactccg tcaaaagaac gcctggacac cccgagcaat 1020
64 gtcccatctc aggagcctga atttgatgcc gccagacttc agacgggtgc gcagacccaa 1080
66 aataaacatg aagatgatga ggatattgtc ccaatttctc actggaagcc gatgcccgaa 1140
68 cggcatccag tcagtccgga ggctttgatc aagctgccaa ccgggcaatc aaaggaactc 1200
70 ccccaactgc aagctaagtt caaggacgag tcgtcctcgg acaagatgca gcggctgcaa 1260
72 caacttgaca ctatcaagtc ggcgttctta catgcgtgga acggttacaa gatctctgcc 1320
74 atgggtcatg atgaggttag acctctgcgc ggtggtttca aggacacatt caatggctgg 1380
76 ggcgcgaccc ttgtcgacgc cttggatacc ctgtggatca tggatctcaa agaggagttc 1440
78 tccatggcag tcgactacgt caagaaaatc gattttacca ccagcaccaa gaaagagatt 1500
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RAW SEQUENCE LISTING　　　　　　　DATE: 09/17/2004
PATENT APPLICATION:　US/10/089,211A　　TIME: 10:04:37

Input Set : A:\62447.txt
Output Set: N:\CRF4\09172004\J089211A.raw

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 82 ggacacaaat acgatatact tttggaaaag tctgttgagc ttgcggatgt cttgatggac   1620
 84 gccttcgaca caccgaaccg gatgccaacc ctctattata aatggagccc agagtatgct   1680
 86 tcagagtttc gccgggggga ctttaaggct gttctcgccg agcttggctc tctctctctc   1740
 88 gagttcacgc gtttggcgca gttgaccaaa caggacaagt actacgatgc aattgcacga   1800
 90 atcacaaatg agctcgaaaa gtatcaggat ttgacaaagc ttcccggctt gtggcctctc   1860
 92 aacctggacg catccgggtg caggcgagtt cccggcgtct cgcgagagcc tgctgcggct   1920
 94 gggcagccag tcagatggtc ctctgacgag atcaactcga cgagctcggt atcgtatcgt   1980
 96 acaagacaaa ttcatgaggg cggagagcct gtccgtcatg acaatgattc gtttgaaacg   2040·
 98 ggttttcctg tatcagtcga tactcggact cctcccccaa agcaagattg caccggaggc   2100
100 ctcaacgatc agctctcagg cattgacaag ttcggactcg gagcccttgg tgactctacg   2160
102 tacgagtact taccgaaaga gtatatgttg ctcggcggta acaacgacca gtacctcaac   2220
104 atgtatcaga aggccatgga cacagtgcga gaatatcttg tttatcagcc aatgctcaag   2280
106 aataatcgcg atgtccgctt cttagcgaca gttagtatga caaagagcct tgatgcaaac   2340
108 cctccggggc gtaccacttt cgcgtacgaa ggcactcacc tcacctgttt tgctggtggt   2400
110 atgcttccca ttggcgccaa gttgtttggg cttgataagg atctaaagct gggtagtcaa   2460
112 ctgacggacg gctgtgtctg ggcatatgaa gccacaaagt ccggaatcat gccggaagca   2520
114 ttccaactgg tcccttgtaa gaaaggcgag ccatgcgaat gggatgagga cgcatactac   2580
116 atggccatgg atccttatgc cgacaagcgg ccaatatcac ataacaaacg ctccgccggc   2640
118 cctgaaaagg ggaattggca cgtcgtcgcc acagccgaat cgtcttcgcc ccaggaagat   2700
120 aaaacacaga aatcaaccac tactgagggt cgacacaccg gtacaactac cggggcaggc   2760
122 gcgctctcgc acgaggaatt cgtcacggga aaaatcctca acgaccgact cccgccgggc   2820
124 atgacaggga tctcggctcg gcagtacctc cttcgcccgg aggcgatcga gtctgtcttc   2880
126 atcatgttcc gcctcacggg cgatccttcc tggcgcgaaa agggttggaa gatgttccag   2940
128 gctgtcgaca aagccacgaa gacggagctg gcgaactcgg ccatttccga cgtaaccgtc   3000
130 gataatccac gcccggtgga cagtatggaa tcattctggc ttgcggagac tctgaaatac   3060
132 ttctaccttc ttttcagcga tccaagcctg gtgagccttg acgaatatgt cttgtaagtg   3120
134 atgcttgact taatcgactg cttgatgctg acttttccct taggaacacc gaggctcatc   3180
136 cgttcaagcg acccaagtac tgaagtacta atttaaatga tcttttagcc tgtatctata   3240
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144 <211> LENGTH: 2448
145 <212> TYPE: DNA
146 <213> ORGANISM: Aspergillus nidulans
148 <220> FEATURE:
149 <221> NAME/KEY: variation
150 <222> LOCATION: (1632)..(1632)
151 <223> OTHER INFORMATION: R = A, C, G, or T
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159 cccgtcgatc accataatcc cccttttcccc gaccagaacc tcaaagatcc atacgaaac   180
161 gacaatagtg cgaccggcag tggggctcct ccgcctgcgt tggtagagcc agaagaatac   240
163 caacgaccac cactttacac agattcagat gacagcccaa ctccgtcaaa agaacgcctg   300·
165 gacaccccga gcaatgtccc atctcaggag cctgaatttg atgccgccag acttcagacg   360
167 ggtgcgcaga cccaaaataa acatgaagat gatgaggata ttgtcccaat ttctcactgg   420
169 aagccgatgc ccgaacggca tccagtcagt ccggaggctt tgatcaagct gccaaccggg   480
171 caatcaaagg aactcccccca actgcaagct aagttcaagg acgagtcgtc ctcggacaag   540
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(handwritten annotation, with circle around "R = A, C, G, or T" and arrow):

Per Sequence Rules, "r" can only represent "a" or "g." Use "n" to represent a, c, g, or t.

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173 atgcagcggc tgcaacaact tgacactatc aagtcggcgt tcttacatgc gtggaacggt  600
175 tacaagatct ctgccatggg tcatgatgag gttagacctc tgcgcggtgg tttcaaggac  660
177 acattcaatg gctggggcgc gacccttgtc gacgccttgg ataccctgtg gatcatggat  720
179 ctcaaagagg agttctccat ggcagtcgac tacgtcaaga aaatcgattt taccaccagc  780
181 accaagaaag agattccggt ctttgaaacc actattcgct acctaggcgg gatgctcggg  840
183 gcctatgata tttcgggaca caaatacgat atacttttgg aaaagtctgt tgagcttgcg  900
185 gatgtcttga tggacgcctt cgacacaccg aaccggatgc caaccctcta ttataaatgg  960
187 agcccagagt atgcttcaga gtttcgccgg ggggacttta aggctgttct cgccgagctt 1020
189 ggctctctct ctctcgagtt cacgcgtttg gcgcagttga ccaaacagga caagtactac 1080
191 gatgcaattg cacgaatcac aaatgagctc gaaaagtatc aggatttgac aaagcttccc 1140
193 ggcttgtggc ctctcaacct ggacgcatcc gggtgcaggc gagttcccgg cgtctcgcga 1200
195 gagcctgctg cggctgggca gccagtcaga tggtcctctg acgagatcaa ctcgacgagc 1260
197 tcggtatcgt atcgtacaag acaaattcat gagggcggag agcctgtccg tcatgacaat 1320
199 gattcgtttg aaacgggttt tcctgtatca gtcgatactc ggactcctcc cccaaagcaa 1380
201 gattgcaccg gaggcctcaa cgatcagctc tcaggcattg acaagttcgg actcggagcc 1440
203 cttggtgact ctacgtacga gtacttaccg aaagagtata tgttgctcgg cggtaacaac 1500
205 gaccagtacc tcaacatgta tcagaaggcc atggacacag tgcgagaata tcttgtttat 1560
207 cagccaatgc tcaagaataa tcgcgatgtc cgcttcttag cgacagttag tatgacaaag 1620
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W--> `209 agccttgatg cnaaacctcc ggggcgtacc actttcgcgt acgaaggcac tcacctcacc 1680`

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213 aagctgggta gtcaactgac ggacggctgt gtctgggcat atgaagccac aaagtccgga 1800
215 atcatgccgg aagcattcca actggtccct tgtaagaaag gcgagccatg cgaatgggat 1860
217 gaggacgcat actacatggc catggatcct tatgccgaca agcggccaat atcacataac 1920
219 aaacgctccg ccggccctga aaaggggaat tggcacgtcg tcgccacagc cgaatcgtct 1980
221 tcgccccagg aagataaaac acagaaatca accactactg agggtcgaca caccggtaca 2040
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225 cgactcccgc cgggcatgac aggatctcg gctcggcagt acctccttcg cccggaggcg 2160
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231 tccgacgtaa ccgtcgataa tccacgcccg gtggacagta tggaatcatt ctggcttgcg 2340
233 gagactctga aatacttcta ccttcttttc agcgatccaa gcctggtgag ccttgaggaa 2400
235 tatgtcttga acaccgaggc tcatccgttc aagcgaccca ggtactga            2448
238 <210> SEQ ID NO: 3
239 <211> LENGTH: 815
240 <212> TYPE: PRT
241 <213> ORGANISM: Aspergillus nidulans
243 <400> SEQUENCE: 3
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249 Phe Val Leu Leu Ile Phe His Phe Ser Arg Leu Ala Val Thr Ile Ser
250              20                  25                  30
253 Leu Gln Ser Trp Val Pro Pro Pro Val Asp His His Asn Pro Pro
254          35                  40                  45
257 Phe Pro Asp Gln Asn Leu Lys Asp Pro Thr Glu Asn Asp Asn Ser Ala
258      50                  55                  60
261 Thr Gly Ser Gly Ala Pro Pro Pro Ala Leu Val Glu Pro Glu Glu Thr
262 65                  70                  75                  80
265 Gln Arg Pro Pro Leu Thr Thr Asp Ser Asp Asp Ser Pro Thr Pro Ser
266              85                  90                  95
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```
269 Lys Glu Arg Leu Asp Thr Pro Ser Asn Val Pro Ser Gln Glu Pro Glu
270          100              105        ,        110
273 Phe Asp Ala Ala Arg Leu Gln Thr Gly Ala Gln Thr Gln Asn Lys His
274          115              120            125
277 Glu Asp Asp Glu Asp Ile Val Pro Ile Ser His Trp Lys Pro Met Pro
278      130              135            140
281 Glu Arg His Pro Val Ser Pro Glu Ala Leu Ile Lys Leu Pro Thr Gly
282 145              150              155                160
285 Gln Ser Lys Glu Leu Pro Gln Leu Gln Ala Lys Phe Lys Asp Glu Ser
286              165              170            175
289 Ser Ser Asp Lys Met Gln Arg Leu Gln Gln Leu Asp Thr Ile Lys Ser
290              180              185            190
293 Ala Phe Leu His Ala Trp Asn Gly Thr Lys Ile Ser Ala Met Gly His
294          195              200            205
297 Asp Glu Val Arg Pro Leu Arg Gly Gly Phe Lys Asp Thr Phe Asn Gly
298      210              215            220
301 Trp Gly Ala Thr Leu Val Asp Ala Leu Asp Thr Leu Trp Ile Met Asp
302 225              230              235                240
305 Leu Lys Glu Glu Phe Ser Met Ala Val Asp Thr Val Lys Lys Ile Asp
306              245              250            255
309 Phe Thr Thr Ser Thr Lys Lys Glu Ile Pro Val Phe Glu Thr Thr Ile
310              260              265            270
313 Arg Thr Leu Gly Gly Met Leu Gly Ala Thr Asp Ile Ser Gly His Lys
314          275              280            285
317 Thr Asp Ile Leu Leu Glu Lys Ser Val Glu Leu Ala Asp Val Leu Met
318      290              295            300
321 Asp Ala Phe Asp Thr Pro Asn Arg Met Pro Thr Leu Thr Thr Lys Trp
322 305              310              315                320
325 Ser Pro Glu Thr Ala Ser Glu Phe Arg Arg Gly Asp Phe Lys Ala Val
326              325              330            335
329 Leu Ala Glu Leu Gly Ser Leu Ser Leu Glu Phe Thr Arg Leu Ala Gln
330              340              345            350
333 Leu Thr Lys Gln Asp Lys Thr Thr Asp Ala Ile Ala Arg Ile Thr Asn
334          355              360            365
337 Glu Leu Glu Lys Thr Gln Asp Leu Thr Lys Leu Pro Gly Leu Trp Pro
338      370              375            380
341 Leu Asn Leu Asp Ala Ser Gly Cys Arg Arg Val Pro Gly Val Ser Arg
342 385              390   .          395                400
345 Glu Pro Ala Ala Ala Gly Gln Pro Val Arg Trp Ser Ser Asp Glu Ile
346              405              410            415
349 Asn Ser Thr Ser Ser Val Ser Thr Arg Thr Arg Gln Ile His Glu Gly
350              420              425            430
353 Gly Glu Pro Val Arg His Asp Asn Asp Ser Phe Glu Thr Gly Phe Pro
354          435              440            445
357 Val Ser Val Asp Thr Arg Thr Pro Pro Pro Lys Gln Asp Cys Thr Gly
358      450              455            460
361 Gly Leu Asn Asp Gln Leu Ser Gly Ile Asp Lys Phe Gly Leu Gly Ala
362 465              470              475                480
365 Leu Gly Asp Ser Thr Thr Glu Thr Leu Pro Lys Glu Thr Met Leu Leu
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RAW SEQUENCE LISTING   DATE: 09/17/2004
PATENT APPLICATION: US/10/089,211A   TIME: 10:04:37

Input Set : A:\62447.txt
Output Set: N:\CRF4\09172004\J089211A.raw

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366                   485              490               495
369 Gly Gly Asn Asn Asp Gln Thr Leu Asn Met Thr Gln Lys Ala Met Asp
370               500              505              510
373 Thr Val Arg Glu Thr Leu Val Thr Gln Pro Met Leu Lys Asn Asn Arg
374           515              520              525
377 Asp Val Arg Phe Leu Ala Thr Val Ser Met Thr Lys Ser Leu Asp Ala
378       530              535              540
381 Asn Pro Pro Gly Arg Thr Thr Phe Ala Thr Glu Gly Thr His Leu Thr
382 545               550              555               560
385 Cys Phe Ala Gly Gly Met Leu Ala Ile Gly Ala Lys Leu Phe Gly Leu
386               565              570              575
389 Asp Lys Asp Leu Lys Leu Gly Ser Gln Leu Thr Asp Gly Cys Val Trp
390           580              585              590
393 Ala Thr Glu Ala Thr Lys Ser Gly Ile Met Pro Glu Ala Phe Gln Leu
394           595              600              605
397 Val Pro Cys Lys Lys Gly Glu Pro Cys Glu Trp Asp Glu Asp Ala Thr
398       610              615              620
401 Thr Met Ala Met Asp Pro Thr Ala Asp Lys Arg Pro Ile Ser His Asn
402 625               630              635               640
405 Lys Arg Ser Ala Gly Pro Glu Lys Gly Asn Trp His Val Val Ala Thr
406               645              650              655
409 Ala Glu Ser Ser Ser Pro Gln Glu Asp Lys Thr Gln Lys Ser Thr Thr
410               660              665              670
413 Thr Glu Gly Arg His Thr Gly Thr Thr Thr Gly Ala Gly Ala Leu Ser
414           675              680              685
417 His Glu Glu Phe Val Thr Gly Lys Ile Leu Asn Asp Arg Leu Pro Pro
418       690              695              700
421 Gly Met Thr Gly Ile Ser Ala Arg Gln Thr Leu Leu Arg Pro Glu Ala
422 705               710              715               720
425 Ile Glu Ser Val Phe Ile Met Phe Arg Leu Thr Gly Asp Pro Ser Trp
426               725              730              735
429 Arg Glu Lys Gly Trp Lys Met Phe Gln Ala Val Asp Lys Ala Thr Lys
430           740              745              750
433 Thr Glu Leu Ala Asn Ser Ala Ile Ser Asp Val Thr Val Asp Asn Pro
434           755              760              765
437 Arg Pro Val Asp Ser Met Glu Ser Phe Trp Leu Ala Glu Thr Leu Lys
438       770              775              780
441 Thr Phe Thr Leu Leu Phe Ser Asp Pro Ser Leu Val Ser Leu Glu Glu
442 785               790              795              800
445 Thr Val Leu Asn Thr Glu Ala His Pro Phe Lys Arg Pro Arg Thr
446               805              810              815
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449 <210> SEQ ID NO: 4
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451 <212> TYPE: DNA
452 <213> ORGANISM: Aspergillus nidulans
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457 ccatcatggg acggtccttg atcctcaagg cacgaagtgg agatcaggtc cgtagtgcat   120
459 atgcatggcc catcagcctg aagcacttcc ccaagcaaag tcgagactcg gacaccgatg   180

<210> SEQ ID NO 15
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<212> TYPE: DNA
<213> ORGANISM: (PCR Primer)
<220> FEATURE:
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<222> LOCATION: (1)..(29)
<223> OTHER INFORMATION:
<400> SEQUENCE: 15
     ggyggyctng gygartcntt ctacgagta   29

invalid <213> response. See item 10 on Error Summary Sheet.

Explanations go on <223> line, not <221> line. See

1.823

same errors in Sequence 16

∴ Sequence Rules.

RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 09/17/2004
PATENT APPLICATION: **US/10/089,211A**   TIME: 10:04:38

Input Set : **A:\62447.txt**
Output Set: **N:\CRF4\09172004\J089211A.raw**

Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220>
to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:2; N Pos. 1632
Seq#:8; N Pos. 4
Seq#:15; N Pos. 9,18
Seq#:16; N Pos. 4,13,16,22,25

Invalid Line Length:

IMPORTANT (see item 2 on Error Summary Sheet)

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:15; Line(s) 812
Seq#:16; Line(s) 827

Input Set : **A:\62447.txt**
Output Set: **N:\CRF4\09172004\J089211A.raw**

L:209 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2 after pos.:1620
L:745 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:0
L:812 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:15
L:817 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:15,Line#:814
L:818 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15 after pos.:0
L:827 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:16
L:832 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:16,Line#:829
L:833 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16 after pos.:0